are described in Altschul *et al., Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al., J. Mol. Biol.* 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

IN THE CLAIMS

Please amend claim 1 as follows. Appendix B provides the "Claims: Version with Markings to Show Changes Made." All pending claims are provided in Appendix C for the Examiner's convenience.

1. (once amended) A method for identifying a compound that modulates signal transduction in sensory cells, the method comprising the steps of:

(i) contacting the compound with a sensory cell specific G-protein alpha subunit polypeptide, the G-protein alpha subunit polypeptide comprising greater than 70% amino acid sequence identity to a polypeptide having a sequence of SEQ ID NO:2; and

(ii) determining a functional effect of the compound upon the G-protein alpha subunit polypeptide, thereby identifying a compound that modulates signal transduction in sensory cells.

REMARKS

Claims 1-4 and 6-8 are pending in the application and have been examined. The rejections are addressed below in the order raised by the Examiners

Restriction Requirement

The election of Group I and species "chemical effect" was made with traverse, as claims 1, 4, and 5 were placed both in Group I and in Group II. Furthermore, claims 23-24, although classified the same class as the claims of Group II, were placed in Group III. As such, on its face this rejection is improper and should be withdrawn. By placing claims 1, 4, and 5 in two separate groups, the Examiner has improperly attempted both to reject these claims for misjoinder, and to reject the claims on the basis that they allegedly represent independent and distinct inventions. Furthermore, examining the claims together would not place an undue examination burden on the Examiner, in particular claims that are in the same class, as are the claims of Groups II and III. As the Examiner has finalized the Restriction